AMENDMENTS TO THE SPECIFICATION

Please replace the first paragraph (lines 2-24) on page 7 with the following amended paragraph:

DNA was isolated from the leaf tissue essentially according to the protocol described earlier (Khanuja SPS, Shasany AK, Darokar MP, Sushil Kumar (1999) Rapid Isolation of PCR Amplifiable DNA from the Dry and Fresh Samples of Plants Producing Large Amounts of Secondary Metabolites and Essential oils by Modified CTAB Procedure. *Plant Molecular Biology Reporter*, **17**, 74.). Polymerase chain reactions (PCRs) were carried out in 25 µl volume. A reaction tube contained 25 ng of DNA, 0.2 unit of Taq DNA polymerase, 100 µM of each dNTPs, 1.5 mM $MgCl_2$, and 5 pmol of decanucleotide primers. The amplifications were carried out using the DNA Engine thermal cycler (MJ Research, USA) using 94°C, 35°C and 72°C temperatures for 40 cycles (Khanuja SPS, Shasany AK, Srivastava A, Sushil Kumar (2000). Assessment of genetic relationships in *Mentha* species. *Euphytica*, **111**, 121-125.). The amplified products were separated on 1.2% agarose gel containing 0.5 µg ml^{-1} of ethidium bromide and photographed with Image master VDS (Pharmacia). The bands were analyzed using Image master ID elite software and the graphic phenogram of the genetic relatedness among the accessions was produced by means of UPGMA (unweighted pair group method with arithmetic average) cluster analysis. Custom-made decanucleotide primers were synthesised in the laboratory on Applied Biosystems 392 DNA-RNA Synthesizer and were designated as MAP01 to MAP20. The sequences of the primers MAP01 to MAP20 were:
AAATCGGAGC (SEQ ID NO: 4), GTCCTACTCG (SEQ ID NO: 5),
GTCCTTAGCG (SEQ ID NO: 6), TGCGCGATCG (SEQ ID NO: 7),
AACGTACGCG (SEQ ID NO: 8), GCACGCCGGA (SEQ ID NO: 9),
CACCCTGCGC (SEQ ID NO: 10), CTATCGCCGC (SEQ ID NO: 11).
CGGGATCCGC (SEQ ID NO: 12), GCGAATTCCG (SEQ ID NO: 13),
CCCTGCAGGC (SEQ ID NO: 14), CCAAGCTTGC (SEQ ID NO: 15),
GTGCAATGAG (SEQ ID NO: 16), AGGATACGTG (SEQ ID NO: 17),
AAGATAGCGG (SEQ ID NO: 18), GGATCTGAAC (SEQ ID NO: 19),
TTGTCTCAGG (SEQ ID NO: 20), CATCCCGAAC (SEQ ID NO: 21),

GGACTCCACG (SEQ ID NO: 22), AGCCTGACGC (SEQ ID NO: 23), respectively.

Please replace the paragraph bridging pages 7 and 8 with the following amended paragraph:

All the RAPD profiles thus generated were analyzed for bands always appearing with all the high artemisinin containing genotypes (more than 0.4%) and absent in the genotypes containing trace or no artemisinin. We could detect a band at approximately 850 base pair region amplified with the primer 5'CCAAGCTTGC3' (~~MAP 12, Sequence ID 1~~SEQ ID NO: 15) which consistently showed its presence in the genotypes containing more than 0.4% artemisinin and absent in the genotypes with trace or no artemisinin. This finding was interesting considering the complex nature of the artemisinin biosynthetic pathway. For all other primers the amplified products showed variable positions in these genotypes and could not be correlated.